BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.17 [Jun-24-2007]

Matrix [BLOSUM62 ▼] gap open: [11] gap extension: [1]
x_dropoff: [0] expect: [10.00] wordsize: [3] Filter [✔] View option [Standard ▼]
Masking character option [X for protein, n for nucleotide ▼] Masking color option
[Black ▼]

[ ] Show CDS translation [Align]

Sequence 1: lcl|1
Length = 116 (1 .. 116)

Sequence 2: lcl|65536
Length = 116 (1 .. 116)
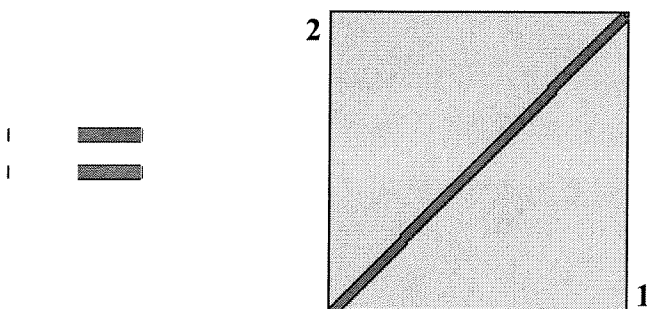
NOTE:Bitscore and expect value are calculated based on the size of the nr database.


```
 Score =  261 bits (666),  Expect = 1e-68
 Identities = 115/116 (99%), Positives = 115/116 (99%), Gaps = 0/116 (0%)

Query  1    SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASWRNSSGTIELVKKGCW  60
            SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASW NSSGTIELVKKGCW
Sbjct  1    SGRGEAETRECIYYNANWELERTNQSGLERCEGEQDKRLHCYASWANSSGTIELVKKGCW  60

Query  61   LDDFNCYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEPPPTAPT  116
            LDDFNCYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEPPPTAPT
Sbjct  61   LDDFNCYDRQECVATEENPQVYFCCCEGNFCNERFTHLPEAGGPEVTYEPPPTAPT  116

CPU time:    0.02 user secs.      0.01 sys. secs       0.03 total secs.
```